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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/627,141	07/25/2003	Juan Carlos de la Torre	TSRI 465.0 D2	4125

26621 7590 02/06/2006

THE SCRIPPS RESEARCH INSTITUTE  
OFFICE OF PATENT COUNSEL, TPC-8  
10550 NORTH TORREY PINES ROAD  
LA JOLLA, CA 92037

EXAMINER

CHEN, STACY BROWN

ART UNIT PAPER NUMBER

1648

DATE MAILED: 02/06/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

**Office Action Summary**

Application No.

10/627,141

Applicant(s)

DE LA TORRE, JUAN CARLOS

Examiner

Stacy B. Chen

Art Unit

1648

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

**Period for Reply**

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

**Status**

- 1) ☒ Responsive to communication(s) filed on 17 November 2005.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

**Disposition of Claims**

- 4) ☒ Claim(s) 5-59 is/are pending in the application.
- 4a) Of the above claim(s) 5-11, 16-27, 31-33 and 35-59 is/are withdrawn from consideration.
- 5) ☐ Claim(s) \_\_\_\_\_ is/are allowed.
- 6) ☒ Claim(s) 12, 28-30 and 34 is/are rejected.
- 7) ☒ Claim(s) 13-15 is/are objected to.
- 8) ☐ Claim(s) \_\_\_\_\_ are subject to restriction and/or election requirement.

**Application Papers**

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☒ The drawing(s) filed on 20 January 2004 is/are: a) ☒ accepted or b) ☐ objected to by the Examiner.  
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).  
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

**Priority under 35 U.S.C. § 119**

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some \* c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
  2. ☐ Certified copies of the priority documents have been received in Application No. \_\_\_\_\_.
  3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).
- \* See the attached detailed Office action for a list of the certified copies not received.

**Attachment(s)**

- |   |   |
|---|---|
| 1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892)   | 4) <input type="checkbox"/> Interview Summary (PTO-413)<br>Paper No(s)/Mail Date. _____ |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948)  | 5) <input type="checkbox"/> Notice of Informal Patent Application (PTO-152)             |
| 3) <input checked="" type="checkbox"/> Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)<br>Paper No(s)/Mail Date <u>11/17/04</u> . | 6) <input checked="" type="checkbox"/> Other: <u>Sequence Alignments</u> .              |

### **DETAILED ACTION**

1. Applicant's amendment filed November 17, 2005 is acknowledged. Claims 5-59 are pending. Claims 5-11, 16-27, 31-33 and 35-59 remain withdrawn from consideration being drawn to non-elected inventions. Claims 12-15, 28-30 and 34 remain under examination. Claim 34 is examined only with respect to the elected subject matter relating to claim 29, from which claim 34 depends. The other embodiments of claim 34 are not under examination.

In the previous Office action, the examiner indicated that SEQ ID NO: 28, 29, 30, 39, 40, 41, 13, 14 and 15 are free of the prior art of record. Upon further consideration and a careful review of the search results, SEQ ID NO: 40 is the only sequence that is free of the prior art of record. On January 20, 2005, the examiner and Michael McCarthy attempted to reach agreement on the claims in view of the examiner's new findings. In the interest of clarifying the record, this Office action is set forth. The examiner regrets any inconvenience to Applicant. In view of the new grounds of rejection, this action is made non-final.

2. A copy of the information disclosure statement PTO-1449 filed October 4, 2004 has been filed on November 17, 2005. The references have been considered, see attached PTO-1449.

### ***Response to Arguments and Amendments***

3. The following objection and rejections are withdrawn:

- The objection to claims 12-15 for minor informalities is withdrawn in view of Applicant's amendment.

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- The rejection of claims 12-15, 28-30 and 34 under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which Applicant regards as the invention, is withdrawn in view of Applicant's amendment.
- The rejection of claims 12-15, 28-30 and 34 are rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claim 7 of U.S. Patent No. 6,057,094, is withdrawn in view of Applicant's filing of a terminal disclaimer over the patented claim(s). The terminal disclaimer is acknowledged and accepted.

***Claim Rejections - 35 USC § 112***

4. (New Rejection) Claim 34 is rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Claim 34 is drawn to a host cell. It is unclear whether the host cell is being referred to *in vitro* or *in vivo*. Suggested language is "An isolated host cell". Correction is required to overcome this rejection.

***Claim Rejections - 35 USC § 102***

5. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

(*New Rejection*) Claims 12, 28-30 and 34 are rejected under 35 U.S.C. 102(b) as being anticipated by Bode *et al.* (*Molecular Psychiatry*, 1996, 1:200-212, “Bode”). The claims are drawn to a substantially purified nucleic acid encoding a human Borna disease virus (BDV) p40 polypeptide consisting essentially of an amino acid residue sequence SEQ ID NO: 28, 29 or 30. The polynucleotides are in vectors which are in host cells. The Office considers “consisting essentially of” to be open claim language. The Office’s interpretation of the claimed invention is a polynucleotide having SEQ ID NO: 28, for example, wherein the polynucleotide has additional nucleotides that do not materially affect the function of SEQ ID NO: 28.

Bode discloses BDV p40 polypeptide sequences that are 190 amino acids in length and have 100% sequence identity to Applicant’s SEQ ID NO: 28, 29 and 30 (see attached Sequence Alignments). SEQ ID NO: 28-30 are all 189 amino acids in length. Bode discloses that the nucleic acid sequences of the p40 polypeptides were obtained and inserted (vector) into an oligodendroglia cell line for expression. (In order for a protein to be expressed, the nucleic acid must have a promoter.) Based on the understanding of “consisting essentially of”, Bode’s polynucleotides read on Applicant’s polynucleotides. The extra amino acid in Bode’s sequence is not expected to materially affect the function of the protein. Thus, the polynucleotide encoding Bode’s protein anticipates Applicant’s claimed polynucleotides.

6. (*New Rejection*) Claims 12, 28-30 and 34 are rejected under 35 U.S.C. 102(b) as being anticipated by WO 96/21021, “WIPO document”. The claims are drawn to a substantially purified nucleic acid encoding a human Borna disease virus (BDV) p40 polypeptide consisting essentially of an amino acid residue sequence SEQ ID NO: 39. The polynucleotides are in

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vectors which are in host cells. The Office considers “consisting essentially of” to be open claim language.

Figure 2 of the WIPO document discloses a polypeptide sequence of 370 amino acids in length that has 100% sequence identity to Applicant’s SEQ ID NO: 39 (see attached Sequence Alignment). Also taught are polynucleotides encoding the polypeptides, wherein the polynucleotides are inserted into a vector and expressed in cells (page 21, lines 12-30). (In order for a protein to be expressed, the nucleic acid must have a promoter.) Based on the understanding of “consisting essentially of”, the polynucleotides of the WIPO document read on Applicant’s polynucleotides. The extra amino acids in the polypeptide sequence are not expected to materially affect the function of the p40 protein, lacking evidence to the contrary.

7. *(New Rejection)* Claim 12 is rejected under 35 U.S.C. 102(b) as being anticipated by Cubitt *et al.* (*Journal of Virology*, 1994, 68(3):1382-1396, “Cubitt”). The claims are drawn to a substantially purified nucleic acid encoding a human Borna disease virus (BDV) p40 polypeptide consisting essentially of an amino acid residue sequence SEQ ID NO: 41. The polynucleotides are in vectors which are in host cells. The Office considers “consisting essentially of” to be open claim language.

Cubitt discloses a polynucleotide sequence encoding a polypeptide sequence of 370 amino acids in length that has 100% sequence identity to Applicant’s SEQ ID NO: 41. SEQ ID NO: 41 is 19 amino acids in length. Based on the understanding of “consisting essentially of”, the polynucleotides Cubitt read on Applicant’s polynucleotides. The extra amino acids in the

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polypeptide sequence are not expected to materially affect the function of the p40 protein encoded by SEQ ID NO: 41, lacking evidence to the contrary.

***Conclusion***

8. No claim is allowed. SEQ ID NO: 40 is free of the prior art of record. Claims 13-15 are objected to for depending from rejected claim 12.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Stacy B. Chen whose telephone number is 571-272-0896. The examiner can normally be reached on M-F (7:00-4:30). If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, James C. Housel can be reached on 571-272-0902. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.



Stacy B. Chen  
February 3, 2006

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 17, 2006, 15:30:13 ; Search time 113.339 Seconds  
(without alignments)  
1176.511 Million cell updates/sec

Title: US-10-627-141-28  
Perfect score: 978  
Sequence: 1 HVTSPSLVLCILIPGLHNA.....TIKEYLACMDATILIPV 189

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%  
Listing first 45 summaries

Database : Uniprot 05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	978	100.0	190	2 Q65468_BDV	Q65468 borna disse
2	970	99.2	370	1 VP40_BDV	Q01552 borna disse
3	970	99.2	370	2 O10395_BDV	O10395 borna disse
4	970	99.2	370	2 O10401_BDV	O10401 borna disse
5	970	99.2	370	2 O5GL86_BDV	O5GL86 borna disse
6	970	99.2	370	2 O5GL92_BDV	O5GL92 borna disse
7	970	99.2	370	2 O5GL95_BDV	O5GL95 borna disse
8	970	99.2	370	2 O5GLC8_BDV	O5GLC8 borna disse
9	970	99.2	370	2 O5GLD1_BDV	O5GLD1 borna disse
10	970	99.2	370	2 O8B29_BDV	O8B29 borna disse
11	970	99.2	370	2 O910H1_BDV	O910H1 borna disse
12	970	99.2	370	2 O91UL4_BDV	O91UL4 borna disse
13	970	99.2	370	2 O91UL8_BDV	O91UL8 borna disse
14	970	99.2	370	2 O774E9_BDV	O774E9 borna disse
15	969	99.1	190	2 O65470_BDV	O65470 borna disse
16	969	99.1	370	2 O10398_BDV	O10398 borna disse
17	966	98.8	370	2 O5GL98_BDV	O5GL98 borna disse
18	964	98.6	370	2 O5GL50_BDV	O5GL50 borna disse
19	964	98.6	370	2 O5GL62_BDV	O5GL62 borna disse
20	964	98.6	370	2 O5GL71_BDV	O5GL71 borna disse
21	964	98.6	370	2 O5GLB3_BDV	O5GLB3 borna disse
22	963	98.5	369	2 O9Q9V1_BDV	O9Q9V1 borna disse
23	960	98.2	370	2 O10392_BDV	O10392 borna disse
24	954	97.5	190	2 O65469_BDV	O65469 borna disse
25	904	92.4	176	2 O77429_BDV	O77429 borna disse
26	904	92.4	176	2 O77430_BDV	O77430 borna disse
27	904	92.4	176	2 O77431_BDV	O77431 borna disse
28	904	92.4	176	2 O77432_BDV	O77432 borna disse
29	904	92.4	176	2 O77433_BDV	O77433 borna disse
30	904	92.4	176	2 O77434_BDV	O77434 borna disse
31	904	92.4	176	2 Q9W8R2_BDV	Q9W8R2 borna disse

32	890	91.0	176	2 Q9WN17_BDV	Q9WN17 borna disse
33	778	79.6	152	2 Q9QCJ2_BDV	Q9QCJ2 borna disse
34	751	76.8	146	2 O12852_BDV	O12852 borna disse
35	751	76.8	146	2 O12853_BDV	O12853 borna disse
36	751	76.8	146	2 O12855_BDV	O12855 borna disse
37	751	76.8	146	2 O12856_BDV	O12856 borna disse
38	751	76.8	146	2 O12857_BDV	O12857 borna disse
39	751	76.8	146	2 O12858_BDV	O12858 borna disse
40	751	76.8	146	2 O12859_BDV	O12859 borna disse
41	751	76.8	146	2 O12860_BDV	O12860 borna disse
42	751	76.8	146	2 O12861_BDV	O12861 borna disse
43	751	76.8	146	2 O12862_BDV	O12862 borna disse
44	751	76.8	146	2 O12863_BDV	O12863 borna disse
45	751	76.8	146	2 O12864_BDV	O12864 borna disse

## ALIGNMENTS

RESULT 1					
ID	Q65468_BDV	PRELIMINARY;	PRT;	190 AA.	
AC	Q65468;				
DT	01-NOV-1996 (TREMBLrel. 01, Created)				
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)				
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DS	P40 (Fragment).				
OS	Borna disease virus (BDV).				
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;				
OC	Bornavirus.				
RX	NCBI_Taxid=12455;				
RX	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RA	MEDLINE=97233300; PubMed=9118344;				
RA	Bode L., Duerrwald R., Rantam F.A., Perszt R., Ludwig H.;				
RT	*First isolates of infectious human Borna disease virus from patients				
RT	with mood disorders.*;				
RL	Mol. Psychiatry 11:200-212 (1996).				
DR	EMBL; U88594; AAB05242.1; -; Genomic_RNA.				
DR	HSSP; Q01552; IN93.				
DR	InterPro; IPR009441; BDV_P40.				
DR	PANTHER; PTHR10207; BDV_P40; 1.				
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FT	NON_TER				
FT	NON_TER				
SQ	SEQUENCE	190 AA; 20896 MW; 75FECAB81370BB9C CRC64;			
Query Match					
Best Local Similarity 100.0%; Score 978; DB 2; Length 190;					
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1 HVTSPSLVLCILIPGLHNAFVHGVPRESYSTPTREGEQVVKAKFYGETTORDLT 60				
DB	1 HVTSPSLVLCILIPGLHNAFVHGVPRESYSTPTREGEQVVKAKFYGETTORDLT 60				
QY	61 ELKISISFHCSCSLIGVIGSSSKIKAGAEQIKRFTMAALNRPSSHGRTATLLQMTN 120				
DB	61 ELKISISFHCSCSLIGVIGSSSKIKAGAEQIKRFTMAALNRPSSHGRTATLLQMTN 120				
QY	121 PHEALDWMNGQPMWVSFLPLITTPESPGRKFMQIKLVASYAQMYYTTTIKEYLACGM 180				
DB	121 PHEALDWMNGQPMWVSFLPLITTPESPGRKFMQIKLVASYAQMYYTTTIKEYLACGM 180				
QY	181 DATLTIPV 189				
DB	181 DATLTIPV 189				
RESULT 2					
ID	VP40_BDV	STANDARD;	PRT;	3 AA.	
AC	Q01552;				
DT	01-JUL-1993 (Rel. 26, Created)				



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:30:13 ; Search time 113.339 Seconds  
(without alignments)  
1176.511 Million cell updates/sec

Title: US-10-627-141-29  
Score: 974  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: UniProt\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	974	100.0	190	2	Q65469_BDV
2	960	98.6	190	2	Q65470_BDV
3	959	98.5	370	1	VP40_BDV
4	959	98.5	370	2	Q10395_BDV
5	959	98.5	370	2	Q10401_BDV
6	959	98.5	370	2	Q5GL86_BDV
7	959	98.5	370	2	Q5GL92_BDV
8	959	98.5	370	2	Q5GL95_BDV
9	959	98.5	370	2	Q5GL98_BDV
10	959	98.5	370	2	Q5GLD1_BDV
11	959	98.5	370	2	Q8B829_BDV
12	959	98.5	370	2	Q910H1_BDV
13	959	98.5	370	2	Q91UH4_BDV
14	959	98.5	370	2	Q91UH6_BDV
15	959	98.5	370	2	Q774E9_BDV
16	959	98.4	370	2	Q10398_BDV
17	955	98.0	370	2	Q5GL98_BDV
18	954	97.9	190	2	Q65468_BDV
19	953	97.8	370	2	Q5GL50_BDV
20	953	97.8	370	2	Q5GL62_BDV
21	953	97.8	370	2	Q5GL71_BDV
22	953	97.8	370	2	Q5GLB3_BDV
23	952	97.7	369	2	Q9Q9V1_BDV
24	949	97.4	370	2	Q10392_BDV
25	893	91.7	176	2	Q77A29_BDV
26	893	91.7	176	2	Q77A30_BDV
27	893	91.7	176	2	Q77A31_BDV
28	893	91.7	176	2	Q77A32_BDV
29	893	91.7	176	2	Q77A33_BDV
30	893	91.7	176	2	Q77A34_BDV
31	893	91.7	176	2	Q9W8R2_BDV

32	879	90.2	176	2	Q9W17_BDV	Q9W17_borna disea
33	767	78.7	152	2	Q9QCJ2_BDV	Q9QCJ2_borna disea
34	740	76.0	146	2	Q12852_BDV	Q12852_borna disea
35	740	76.0	146	2	Q12853_BDV	Q12853_borna disea
36	740	76.0	146	2	Q12855_BDV	Q12855_borna disea
37	740	76.0	146	2	Q12856_BDV	Q12856_borna disea
38	740	76.0	146	2	Q12857_BDV	Q12857_borna disea
39	740	76.0	146	2	Q12858_BDV	Q12858_borna disea
40	740	76.0	146	2	Q12859_BDV	Q12859_borna disea
41	740	76.0	146	2	Q12860_BDV	Q12860_borna disea
42	740	76.0	146	2	Q12861_BDV	Q12861_borna disea
43	740	76.0	146	2	Q12862_BDV	Q12862_borna disea
44	740	76.0	146	2	Q12863_BDV	Q12863_borna disea
45	740	76.0	146	2	Q12864_BDV	Q12864_borna disea

## ALIGNMENTS

RESULT 1	ID	Q65469_BDV	PRELIMINARY;	PRT;	190 AA.
AC	Q65469;				
DT	01-NOV-1996	(Tremblrel. 01, Created)			
DT	01-NOV-1996	(Tremblrel. 01, Last sequence update)			
DT	01-MAR-2004	(Tremblrel. 26, Last annotation update)			
DE	P40 (Fragment).				
OS	Borna disease virus (BDV).				
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;				
OX	Bornavirus.				
NCBI	Taxid=12455;				
[1]					
RP	NCBIROTIDE SEQUENCE.				
FX	MEDLINE=97233300; Pubmed=918344;				
RA	Bode U., Duerwald R., Rantam P.A., Petzert R., Ludwig H.;				
RT	"First isolates of infectious human Borna disease virus from patients				
RT	with mood disorders.";				
RL	Mol. Psychiatry 1:200-212 (1996).				
DR	EMBL; U56595; AB05243.1; -; Genomic_RNA.				
DR	HSP; Q01552; IN93.				
DR	InterPro; IPR009441; BDV_P40.				
DR	PANTHER; PTHR10207; BDV_P40; 1.				
DR	Pfam; PF06407; BDV_P40; 1.				
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FT	NON_TER	1			
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Query Match		100.0%;	Score 974;	DB 2;	Length 190;
Best Local Similarity		100.0%;	Pred. No. 2.9e-84;		
Matches	189;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
QY	1	HTVPSIVFLCLIPGLHAAFHGCVPRSTSLPTIRGEQTVKTAFFYEKTTORDLT	60		
DB	1	HTVPSIVFLCLIPGLHAAFHGCVPRSTSLPTIRGEQTVKTAFFYEKTTORDLT	60		
QY	61	ELEISSTFSHCSSLIGVVGSSSKIRAEAOIKRRPTWMAAANRSHGSTATLLQWEN	120		
DB	61	ELEISSTFSHCSSLIGVVGSSSKIRAEAOIKRRPTWMAAANRSHGSTATLLQWEN	120		
QY	121	PHEAIDWINGQPMWGSFVLSLTATDFSPGKEFMDQIKLVASVQMTTYTIIKEYLAECM	180		
DB	121	PHEAIDWINGQPMWGSFVLSLTATDFSPGKEFMDQIKLVASVQMTTYTIIKEYLAECM	180		
QY	181	DATLTIPV 189			
DB	181	DATLTIPV 189			
RESULT 2					
ID	Q65470_BDV	PRELIMINARY;	PRT;	190 AA.	
AC	Q65470;				
DT	01-NOV-1996	(Tremblrel. 01, Created)			



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:28:28 / Search time 11.9228 Seconds  
(without alignments)  
663.334 Million cell updates/sec

Title: US-10-627-141-39

Perfect score: 95  
Sequence: 1 MPKRLVDDADAMEDQD 18

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database:

A\_Geneseq\_21:\*

- 1: geneeqp1980s:\*
- 2: geneeqp1990s:\*
- 3: geneeqp2000s:\*
- 4: geneeqp2001s:\*
- 5: geneeqp2002s:\*
- 6: geneeqp2003as:\*
- 7: geneeqp2003bs:\*
- 8: geneeqp2004s:\*
- 9: geneeqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	18	2	AAW49061 Human Bor
2	95	100.0	370	2	AAW49061 Human Bor
3	83	87.4	18	8	ADST5684 Borna dis
4	48.5	51.1	567	8	ADST5684 Borna dis
5	48	50.5	345	8	AE827254 Bacterial
6	48	50.5	736	8	ADY10076 Plant ful
7	48	50.5	736	8	ADY10076 Plant ful
8	48	50.5	1134	7	ADST7084 Plant ful
9	48	50.5	1526	4	AAW79777 Human pro
10	48	50.5	1526	4	AAW79777 Human pro
11	48	50.5	1526	4	ABG06116 Novel hum
12	48	50.5	1552	4	AAW78793 Human pro
13	48	50.5	1554	4	ABG07288 Novel hum
14	48	50.5	1584	4	ABG07290 Novel hum
15	48	50.5	1627	4	ABG06117 Novel hum
16	48	50.5	1881	2	AAW24025 Amino aci
17	48	48.4	131	3	AAW6712 Membrane-
18	48	48.4	131	3	AAW57844 Human lep
19	48	48.4	131	3	AAW03730 OB-RGR2
20	48	48.4	131	3	AAW94849 Human pro
21	48	48.4	131	4	AAU29127 Human pro
22	48	48.4	131	4	AAW88337 Human mem
23	48	48.4	131	4	AAW55235 Human pro
24	48	48.4	131	5	ABW89581 Human pol

25	46	48.4	131	5	ABB84894	ABW84894 Human PRO
26	46	48.4	131	5	ABB95500	ABW95500 Human ang
27	46	48.4	131	6	ABU85803	ABU85803 Human PRO
28	46	48.4	131	6	ABU88051	ABU88051 Novel hum
29	46	48.4	131	6	ABU84366	ABU84366 Human sec
30	46	48.4	131	6	ABR66240	ABR66240 Human sec
31	46	48.4	131	6	ABR65630	ABR65630 Human sec
32	46	48.4	131	6	ABU99570	ABU99570 Human sec
33	46	48.4	131	6	ABU8050	ABU8050 Human PRO
34	46	48.4	131	6	ABU59128	ABU59128 Novel hum
35	46	48.4	131	6	ABU82640	ABU82640 Human sec
36	46	48.4	131	6	ABU82809	ABU82809 Human PRO
37	46	48.4	131	6	ABU89930	ABU89930 Novel hum
38	46	48.4	131	6	ABR68179	ABR68179 Human sec
39	46	48.4	131	6	ABU60559	ABU60559 Human sec
40	46	48.4	131	6	ABU96232	ABU96232 Novel hum
41	46	48.4	131	6	ABU92663	ABU92663 Human sec
42	46	48.4	131	6	ABO08740	ABO08740 Human sec
43	46	48.4	131	6	ABO02792	ABO02792 Human sec
44	46	48.4	131	6	ABR74946	ABR74946 Human sec
45	46	48.4	131	6	ABR94708	ABR94708 Human sec

#### ALIGNMENTS

RESULT 1  
AAW49061 standard; peptide, 18 AA.

AAW49061:  
27-AUG-2003 (revised)  
09-NOV-1998 (first entry)

Human Borna disease virus p40 peptide.  
BDV, infection; diagnosis; neuropsychiatric disorder; human.  
Borna disease virus.  
W09830238-A1.  
16-JUL-1998.  
07-JAN-1998; 98WO-US000495.  
07-JAN-1997; 97US-00779764.  
(SCRI) SCRIPPS RES INST.  
De La Torre JC;  
WPI; 1998-398802/34.  
New isolated human Borna disease nucleic acid(s) - which encode p24, p16, p56, p40 and L polymerase catalytic domain poly:peptide(s), used to develop products for detection.  
Claim 5; Page 165; 207pp; English.

This peptide is characteristic of novel p40 proteins (see AAW49051-53) of human Borna disease virus (BDV) isolates obtained from psychiatric patients. The invention provides nucleic acids (see AAW2840-55) that encode BDV p24, p16, p56, p40 and L polymerase catalytic domain polypeptides (see AAW49043-63) obtained from psychiatric patients (isolates H1, H2 and H3) as well as from non-human BDV strain V. Also provided are expression vectors, transformed host cells and antibodies raised against the human BDV polypeptides. Human BDV polypeptides, polynucleotides and antibodies can be used in claimed methods for detecting human BDV or human BDV-like viral infection, particularly in patients with neuropsychiatric disorders. (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 18 AA;  
SQ

Query Match 100.0%; Score 95; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.4e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPPKRLVDDADAMEDD 18  
DB 1 MPPKRLVDDADAMEDD 18

RESULT 2  
ID AAR98617 standard; protein; 370 AA.  
XX AAR98617;

XX 16-OCT-2003 (revised)  
DT 10-DEC-1996 (first entry)  
XX

DE Borna disease virus p40.

XX Borna disease virus; BDV; p40; nervous system disease;  
KM neuro-psychiatric disease; schizophrenia; diagnosis; therapy; vaccine;  
XX antibody.

XX Borna disease virus; strain V.

XX WO9621020-A2.

XX 11-JUL-1996.

XX 05-JAN-1996; 96WO-US000418.

XX 06-JAN-1995; 95US-00369822.

XX 04-MAY-1995; 95US-00434831.

XX 04-JAN-1996; 96US-00582776.

XX (REGC) UNIV CALIFORNIA.

XX Lipkin WJ, Briese T, Kliche S, Schneider PA, Stitz L;  
PI Schneemann A;  
XX

DR WPI: 1996-333995/33.

DR N-PSDB; AAT38104.

PT Borna disease virus (BDV) nucleotide and protein sequences - useful for  
PT the diagnosis and treatment of infection and non-BDV related neuro-logic  
PT and neuro-psychiatric disease.

XX Disclosure; Fig 2; 186pp; English.

XX Borna disease virus (BDV) p40 (AAR98617) was identified from an ORF on  
CC the virus antigenome strand (AAT38104). p40 is expressed at high levels  
CC in vitro and in vitro and is found in the nucleus and cytoplasm of BDV-  
CC infected cells. Recombinant p40 was obtd. by PCR amplification (see also  
CC AAT38113) of the p40 coding sequence and expression in Escherichia coli  
CC transformants. It was used with BDV p23 (AAR98618) and gp18 (AAR98603) in  
CC an ELISA for the detection of BDV antibodies. (Updated on 16-OCT-2003 to  
CC standardise OS field)

XX Sequence 370 AA;

Query Match 100.0%; Score 95; DB 2; Length 370;  
Best Local Similarity 100.0%; Pred. No. 6.2e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPPKRLVDDADAMEDD 18  
DB 1 MPPKRLVDDADAMEDD 18

RESULT 3  
AD575684  
ID AD575684 standard; peptide; 18 AA.  
XX AD575684;

XX 02-DEC-2004 (first entry)  
DT

DE Borna disease virus p40 protein fragment #1 for detecting BDV infections.

XX detection; exogenous antigen; class switching; IgM; IgG; immunoglobulin;  
KM BDV; Borna disease virus; p24.

XX Borna disease virus.

XX EPI460426-A1.

XX 22-SEP-2004.

XX 19-MAR-2004; 2004BP-00006699.

XX 20-MAR-2003; 2003JP-00078898.

XX 26-MAR-2003; 2003JP-00086490.

XX 26-MAR-2003; 2003JP-00086491.

XX (SYSM-) SYSMEX CORP.

XX Yamauchi K, Horii Y, Takahama Y, Negai S;  
PI WPI: 2004-679696/67.

PT Detecting antibody against exogenous antigen e.g. Borna disease virus  
PT (BDV), involves detecting the IgM antibody to the exogenous antigen.

XX Claim 14; SEQ ID NO 3; 33pp; English.

XX The invention relates to a method of detecting (M1) an antibody, where an  
CC examination of a disease caused by an exogenous antigen is conducted, the  
CC exogenous antigen being an antigen having a property in which the class  
CC switching from the IgM antibody to the IgG antibody of immunoglobulin  
CC antibodies raised against the antigen is achieved after two months  
CC following the appearance of the IgM antibody, the method involves  
CC detecting the IgM antibody to the exogenous antigen. The specification  
CC also discloses a reagent (I) for detecting an anti-BDV antibody,  
CC comprising an antigen polypeptide selected from the p10 region of a Borna  
CC disease virus (BDV) protein. (M1) is useful for detecting an antibody  
CC specific to an exogenous antigen. The exogenous antigen is a  
CC microorganism, virus and/or proteinaceous substance, which may be the  
CC cause of a disease of a human or of a mammal other than humans. The  
CC exogenous antigen is preferably Borna disease virus (BDV). (I) is useful  
CC for detecting anti-BDV antibody. (M1) is accurate and enables the  
CC measurement of an antibody also in the early stage of the infection. (M1)  
CC has high detection sensitivity. This sequence corresponds to a peptide  
CC antigen from the BDV p40 protein and used in the method of the invention.

XX Sequence 18 AA;

Query Match 87.4%; Score 83; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.2e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PKRRLVDDADAMEDD 18  
DB 1 PKRRLVDDADAMEDD 16

RESULT 4  
ID ADS43695

XX ADS43695 standard; protein; 567 AA.

XX ADS43695;

DT 02-DEC-2004 (first entry)

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:30:13 ; Search time 11.3939 Seconds  
(without alignments)  
1176.511 Million cell updates/sec

Title: US-10-627-141-41

Perfect score: 88

Sequence: 1 ELSEISAIIRMGIVTGLV 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UnIProt\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	95.5	370	1	VP40_BDV
2	84	95.5	370	1	VP40_BDV
3	81	92.0	369	2	Q9Q9V1_BDV
4	81	92.0	370	2	Q10392_BDV
5	81	92.0	370	2	Q10395_BDV
6	81	92.0	370	2	Q10401_BDV
7	81	92.0	370	2	Q5GL50_BDV
8	81	92.0	370	2	Q5GL62_BDV
9	81	92.0	370	2	Q5GL71_BDV
10	81	92.0	370	2	Q5GL92_BDV
11	81	92.0	370	2	Q5GL95_BDV
12	81	92.0	370	2	Q5GL98_BDV
13	81	92.0	370	2	Q5GLB3_BDV
14	81	92.0	370	2	Q5GLC8_BDV
15	81	92.0	370	2	Q8B829_BDV
16	81	92.0	370	2	Q910H1_BDV
17	81	92.0	370	2	Q91UD4_BDV
18	81	92.0	370	2	Q91UJ8_BDV
19	81	90.9	370	2	Q10398_BDV
20	80	90.9	370	2	Q5GL86_BDV
21	80	90.9	370	2	Q5GLD1_BDV
22	48	54.5	123	2	Q8TM18_METAC
23	48	54.5	256	2	Q9AMB8_9POL
24	48	54.5	358	2	Q5JDP0_PYRO
25	47	53.4	188	2	Q8ZYR2_PYRA
26	47	53.4	254	2	Q81590_ANOMA
27	47	53.4	255	2	Q81558_9POL
28	47	53.4	373	2	Q7N116_GLOVI
29	47	53.4	537	2	Q522N2_MAGGR
30	46	52.3	90	2	Q513B4_MONAL
31	46	52.3	244	2	Q81539_3POL

32	46	52.3	246	2	Q81560_ZEALU
33	46	52.3	247	2	Q81596_METCU
34	46	52.3	248	2	Q6UT05_3POL
35	46	52.3	249	2	Q6UT02_TAECM
36	46	52.3	249	2	Q6UT07_9POL
37	46	52.3	249	2	Q6UT08_9POL
38	46	52.3	249	2	Q6UTV1_9POL
39	46	52.3	249	2	Q6UTV2_9POL
40	46	52.3	249	2	Q6UTV4_9POL
41	46	52.3	249	2	Q6UTV5_9POL
42	46	52.3	249	2	Q6UTV6_9POL
43	46	52.3	249	2	Q6UTV8_9POL
44	46	52.3	249	2	Q6UTW0_9POL
45	46	52.3	249	2	Q6UTW4_9POL
					Q6UTW4 elymus repe

## ALIGNMENTS

RESULT 1  
VP40\_BDV STANDARD; PRT; 370 AA.  
ID VP40\_BDV  
AC Q01552;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE 40 kDa protein.  
GN Name=P40; Synonyms=P38;  
OS Borna disease virus (BDV).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;  
OC Bornaviruses.  
OX NCBI\_TaxID=12455;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C6;  
RX MEDLINE=94149825; PubMed=7906311;  
RA Cubitt B., Oldstone C., de la Torre J.C.;  
RT "Sequence and genome organization of Borna disease virus.";  
RL J. Virol. 68:1382-1396(1994).  
RN [2]  
RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.  
RC STRAIN=Clone B8;  
RX MEDLINE=93303922; PubMed=8317098;  
RA Pyper J.M., Richt J.A., Brown L., Rott R., Narayan O., Clements J.E.;  
RT "Genomic organization of the structural proteins of Borna disease virus revealed by a cDNA clone encoding the 38-kDa protein.";  
RL Virology 195:229-238(1993).  
RN [3]  
RP NUCLEOTIDE SEQUENCE OF 10-370.  
RC STRAIN=Gieszen / HE/80-3;  
RA Blinz T., Riehle H., Yamaaki J., Richt J.A., Grebenstein O., Rott R.,  
RL Nienmann H.;  
RT Submitted (SEP-1992) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Halle B1/91;  
RX MEDLINE=94076462; PubMed=8254777;  
RA Schneider P.A., Briese T., Zimmermann W., Ludwig H., Lipkin W.I.;  
RT "Sequence conservation in field and experimental isolates of Borna disease virus.";  
RL J. Virol. 68:63-68(1994).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=V;  
RX MEDLINE=94240137; PubMed=8183914;  
RA Briese T., Schneemann A., Lewis A.J., Park Y.-S., Kim S., Ludwig H.,  
RL Lipkin W.I.;  
RT "Genomic organization of Borna disease virus.";  
RN [6]  
RP Proc. Natl. Acad. Sci. U.S.A. 91:4362-4366(1994).  
RN NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.  
RC STRAIN=HR/80-1;  
RX MEDLINE=93021385; PubMed=1404604;

RA McClure M.A., Thibault K.J., Hatalski C.G., Lipkin W.I.;  
 RT "sequence similarity between Borna disease virus p40 and a duplicated  
 RT domain within the paramyxovirus and rhabdovirus polymerase proteins";  
 RL J. Virol. 66:6572-6577(1992).  
 CC -1- FUNCTION: Could be involved in the transport of nucleoprotein  
 CC particles from the nucleus to the cytoplasm.  
 CC -1- SUBCELLULAR LOCATION: Nucleus and cytoplasm of the infected cells.  
 CC CAUTION: It is uncertain whether Met-1 or Met-14 is the initiator.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC  
 DR EMBL: L27077; AAA20663.1; -; Genomic RNA.  
 DR EMBL: S62821; AAB27261.1; ALT\_INIT; Genomic\_RNA.  
 DR EMBL: X68392; CAA48458.1; ALT\_INIT; mRNA.  
 DR EMBL: S67502; AAB29214.1; -; Genomic\_RNA.  
 DR EMBL: U04608; AAA20224.1; -; Genomic\_RNA.  
 DR EMBL: M99375; AAA73385.1; ALT\_INIT; mRNA.  
 DR PDB: 1N93; X-ray; K=1-370.  
 DR PDB: 1EP1; X-ray; K=1-370.  
 DR InterPro: IPR009441; BDV\_P40.  
 DR PANTHER: PTHR10207; BDV\_P40; 1.  
 DR Pfam: PF06407; BDV\_P40; 1.  
 KM 3D-structure: Direct protein sequencing.  
 FT VARIANT 47 47 I -> T (in strain HE/80-1).  
 FT VARIANT 56 56 N -> S (in strain Halle BI/91).  
 FT VARIANT 275 275 E -> D (in strain V).  
 FT VARIANT 357 357 I -> V (in strain Halle BI/91).  
 FT VARIANT 362 362 R -> K (in strain Halle BI/91 and strain  
 FT V).  
 FT CONFLICT 1 1 M -> L (in Ref. 6).  
 SQ SEQUENCE 370 AA; 40981 MW; C02454BDABSE4E53 CRC64;  
 Query Match 95.5%; Score 84; DB 1; Length 370;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-05;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ELSGEISAIMRMIGVTGL 18  
 DB 352 ELSGEISAIMRMIGVTGL 369  
 RESULT 2  
 Q774E9 BDV PRELIMINARY; PRT; 370 AA.  
 ID Q774E9 BDV PRELIMINARY; PRT; 370 AA.  
 AC Q774E9;  
 DT 10-MAY-2005 (TREMBLrel. 30. Created)  
 DT 10-MAY-2005 (TREMBLrel. 30. Last sequence update)  
 DT 10-MAY-2005 (TREMBLrel. 30. Last annotation update)  
 DE P40 protein (Nucleoprotein).  
 OS Borna disease virus (BDV).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;  
 OC Bornavirus.  
 OX NCBI\_TaxID=12455;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=CRP3A, CRP3B, and CRNP5;  
 RX MEDLINE=22153693; PubMed=12163584;  
 RX DOI=10.1128/JVI.76.17.8650-8658.2002;  
 RA Mishino Y., Kobasa D., Rubin S.A., Pletnikov M.V., Carbone K.M.;  
 RT "Enhanced neurovirulence of borna disease virus variants associated  
 RT with nucleotide changes in the glycoprotein and L polymerase genes";  
 RL J. Virol. 76:8650-8658(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=21488520; PubMed=11602780;  
 RA Pleschka S., Staeheli P., Kolodziejek J., Richt J.A., Nowotny N.,  
 RA Schwemmler M.;  
 RT "Conservation of coding potential and terminal sequences in four  
 RT different isolates of Borna disease virus";

RL J. Gen. Virol. 82:2681-2690(2001).  
 DR EMBL: AY114161; AAM68134.1; -; Genomic\_RNA.  
 DR EMBL: AY114162; AAM68140.1; -; Genomic\_RNA.  
 DR EMBL: AY114163; AAM68146.1; -; Genomic\_RNA.  
 DR EMBL: AJ311522; CAC70640.1; -; Genomic\_RNA.  
 KM Viral nucleoprotein.  
 SQ SEQUENCE 370 AA; 40981 MW; C02454BDABSE4E53 CRC64;  
 Query Match 95.5%; Score 84; DB 2; Length 370;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-05;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ELSGEISAIMRMIGVTGL 18  
 DB 352 ELSGEISAIMRMIGVTGL 369  
 RESULT 3  
 Q909V1 BDV PRELIMINARY; PRT; 369 AA.  
 ID Q909V1 BDV PRELIMINARY; PRT; 369 AA.  
 AC Q909V1;  
 DT 01-MAY-2000 (TREMBLrel. 13. Created)  
 DT 01-MAY-2000 (TREMBLrel. 13. Last sequence update)  
 DT 01-FEB-2005 (TREMBLrel. 29. Last annotation update)  
 DE N protein (Nucleoprotein).  
 OS Borna disease virus (BDV).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;  
 OC Bornavirus.  
 OX NCBI\_TaxID=12455;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=No/98;  
 RX MEDLINE=20283825; PubMed=10823873;  
 RX DOI=10.1128/JVI.74.12.5655-5658.2000;  
 RA Nowotny N., Kolodziejek J., Jehle C.O., Suchy A., Staeheli P.,  
 RA Schwemmler M.;  
 RT "Isolation and characterization of a new subtype of Borna disease  
 RT virus";  
 RL J. Virol. 74:5655-5658(2000).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=No/98;  
 RX MEDLINE=21488520; PubMed=11602780;  
 RA Pleschka S., Staeheli P., Kolodziejek J., Richt J.A., Nowotny N.,  
 RA Schwemmler M.;  
 RT "Conservation of coding potential and terminal sequences in four  
 RT different isolates of Borna disease virus";  
 RL J. Gen. Virol. 82:2681-2690(2001).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=No/98;  
 RX MEDLINE=21488520; PubMed=11602780;  
 RA Nowotny N., Kolodziejek J., Jehle C.O., Suchy A., Staeheli P.,  
 RA Schwemmler M.;  
 RT "Isolation and characterization of a new subtype of Borna disease  
 RT virus";  
 RL J. Gen. Virol. 82:2681-2690(2001).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=No/98;  
 RA Nowotny N., Kolodziejek J.;  
 RT "Isolation and characterization of a new subtype of Borna disease  
 RT virus";  
 RL J. Gen. Virol. 74:5655-5658(2000).  
 DR EMBL: AF136236; AAF22169.1; -; Genomic\_RNA.  
 DR EMBL: AJ311524; CAC70654.1; -; Genomic\_RNA.  
 DR HSSP: Q01552; 1N93.  
 DR InterPro: IPR009441; BDV\_P40.  
 DR PANTHER: PTHR10207; BDV\_P40; 1.  
 DR Pfam: PF06407; BDV\_P40; 1.  
 KM Viral nucleoprotein.  
 SQ SEQUENCE 369 AA; 40930 MW; 9A5C9A95720F3BP9 CRC64;